

09900102-112101

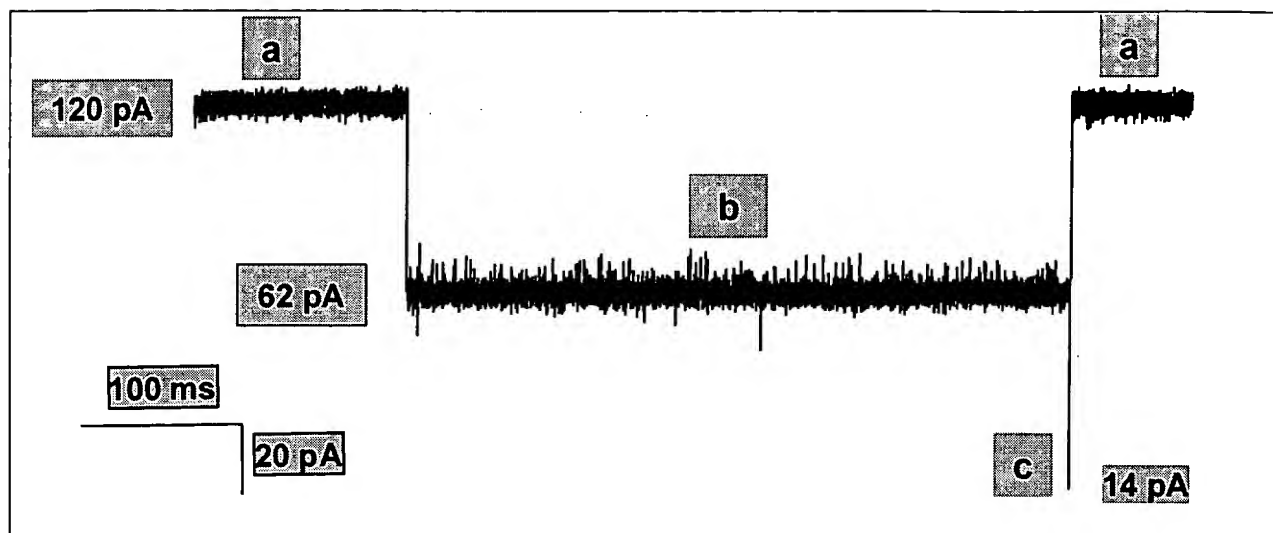


Figure 1

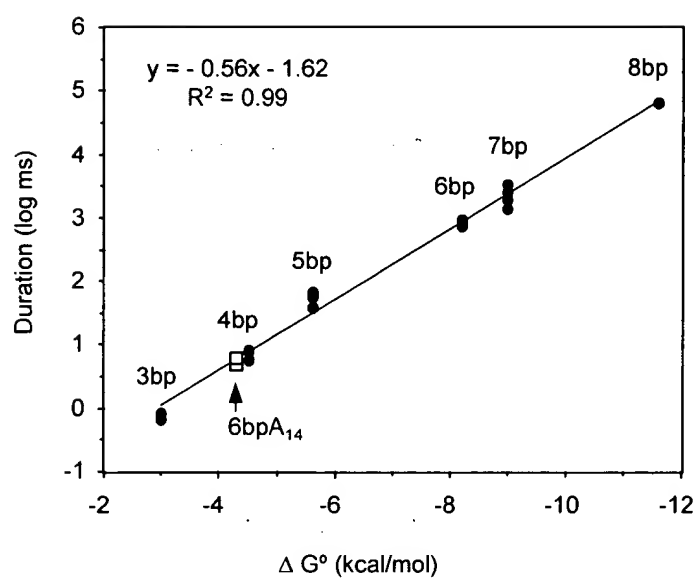


Figure 2

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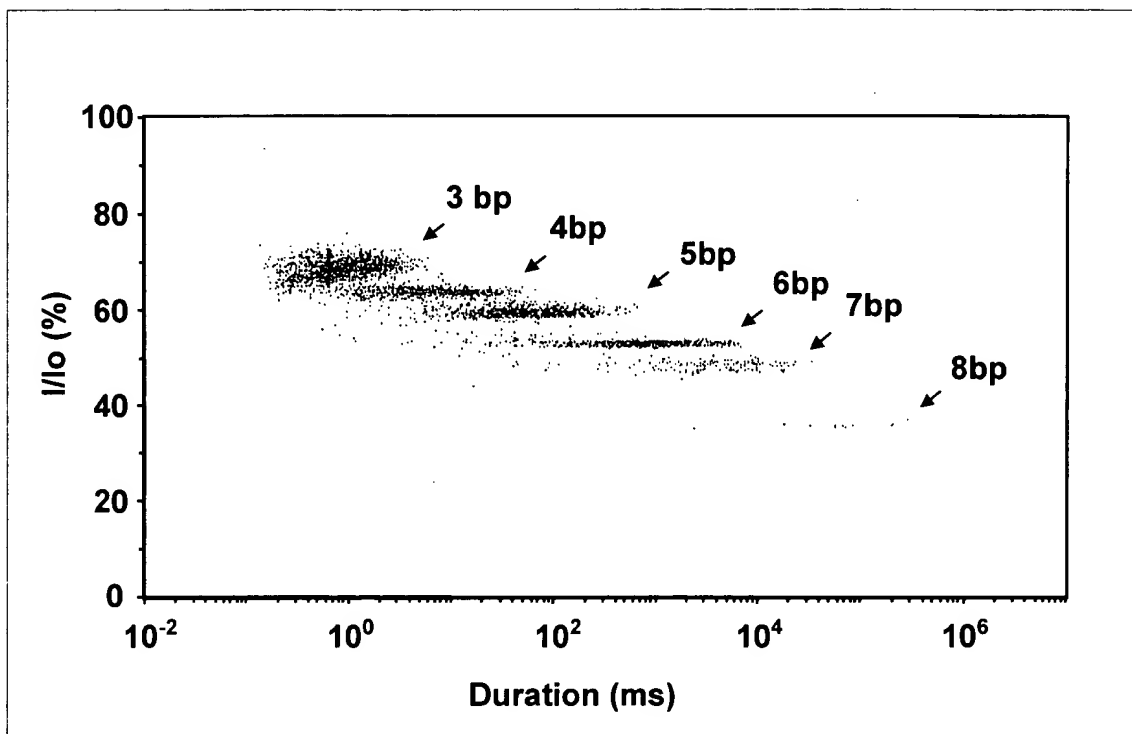


Figure 3a

A histogram showing the distribution of SVM Scores for 1000 random samples. The x-axis is labeled 'SVM Score' and ranges from -3.0 to 3.0. The y-axis is labeled 'Number of Events' and is on a logarithmic scale from 1 to 1000. A vertical dashed line at approximately 0.75 marks the 'Rejection Region'. The distribution is bimodal, with a peak around -1.0 and a smaller peak around 1.2.



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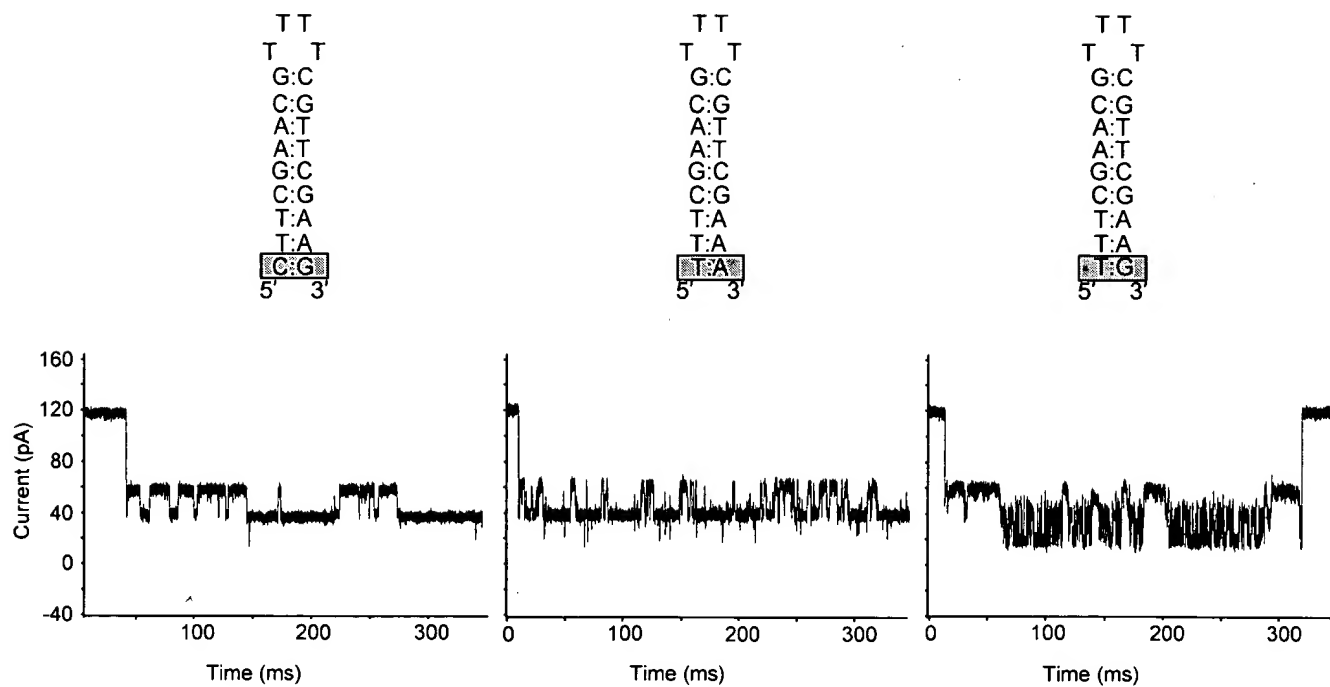


Figure 3c

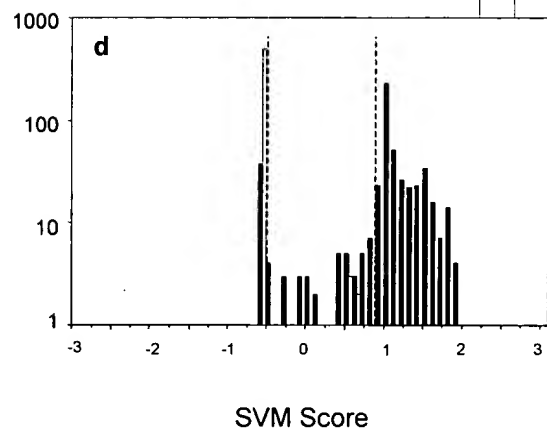
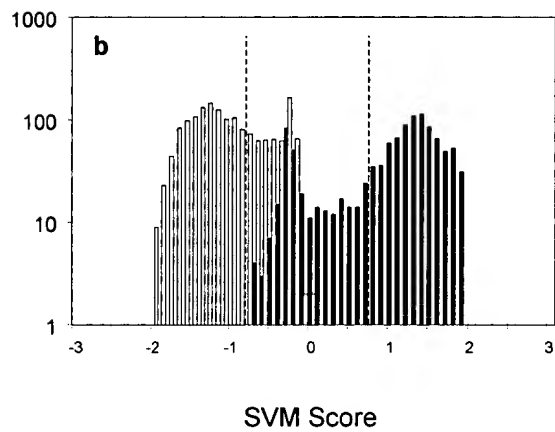
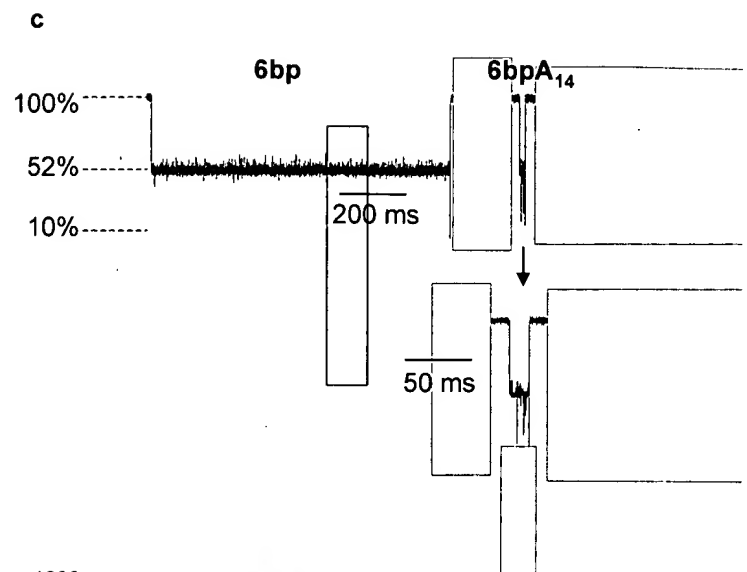
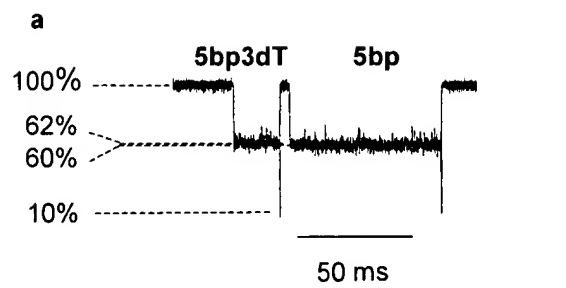


Figure 4

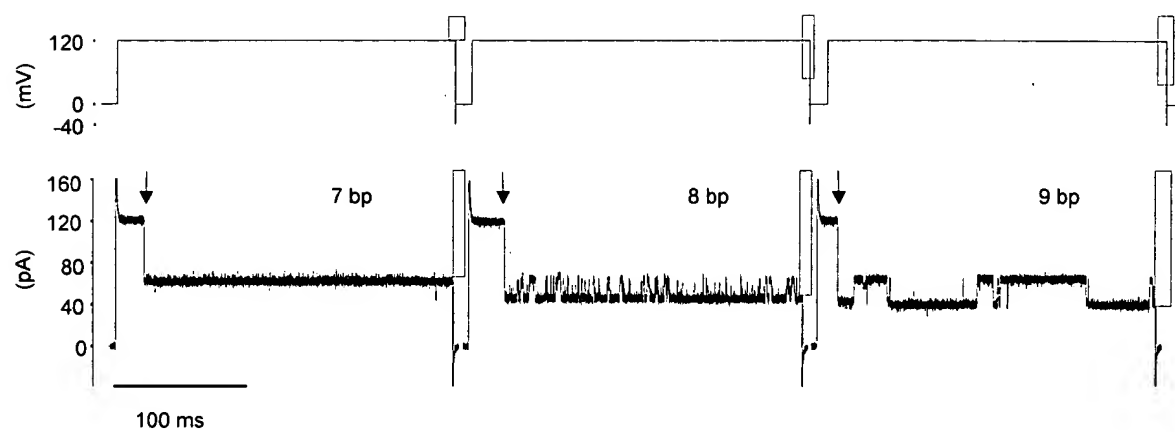
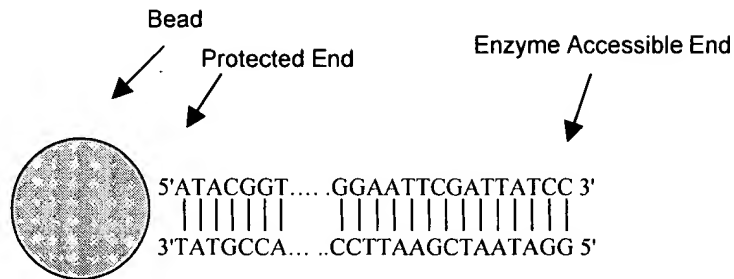


Figure 5

Figure 6.

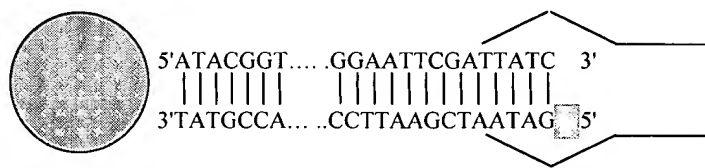
A) Blunt-ended DNAs are attached at one end to a bead.



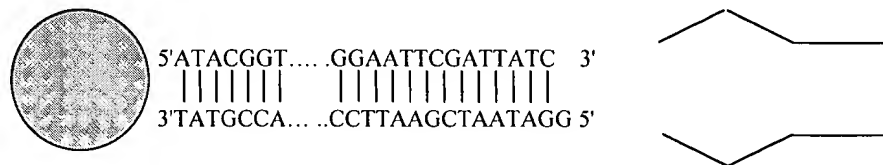
B) A single nucleotide is cut from the 3' end by a low processivity exonuclease such as exonuclease III.



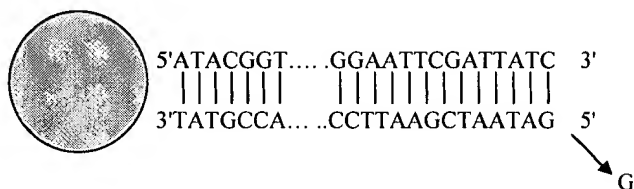
C) The single nucleotide overhang at the 5' end is read when the duplex end is captured in the nanopore under an applied voltage.



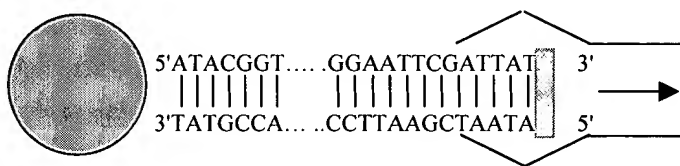
D) Once read, the DNA duplex is released from the nanopore by reversing the applied voltage.



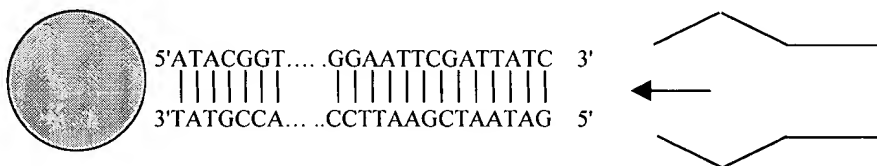
E) The single-nucleotide overhang is then cut with a nuclease (such as mung bean exonuclease), resulting in a blunt end.

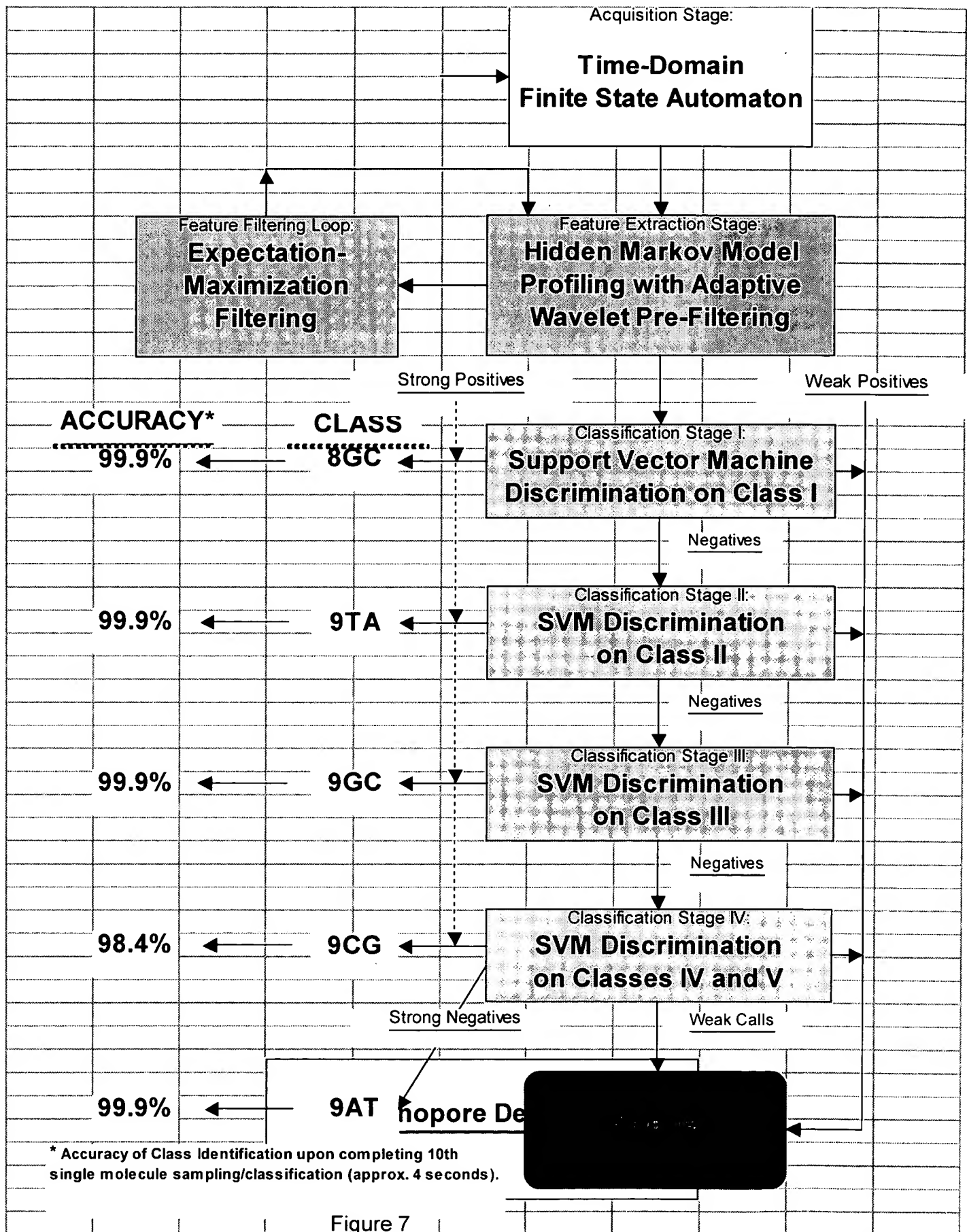


F) The blunt end is then captured and held in the nanopore by an applied voltage. The terminal base-pair is identified while the duplex is captured.



G) Once read, the DNA duplex is released from the nanopore by reversing the applied voltage. The cycle is then repeated at step B).





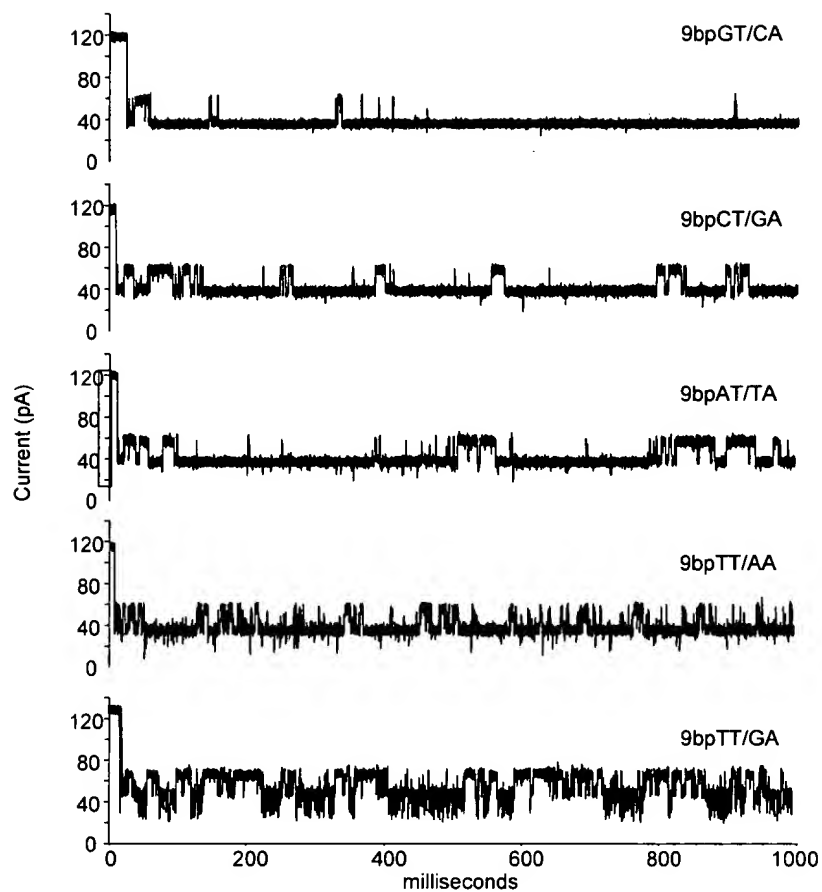


Figure 9

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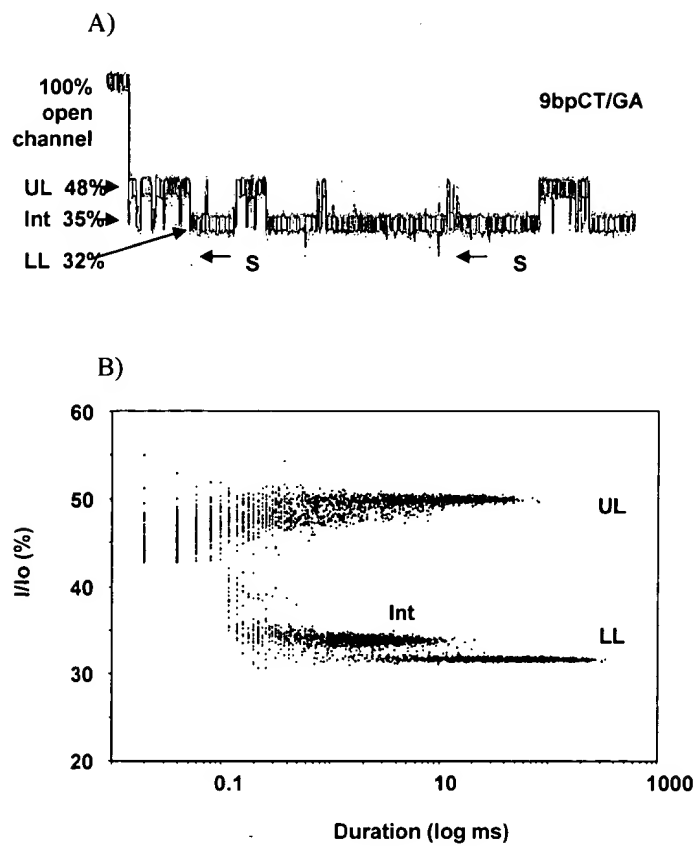


Figure 10

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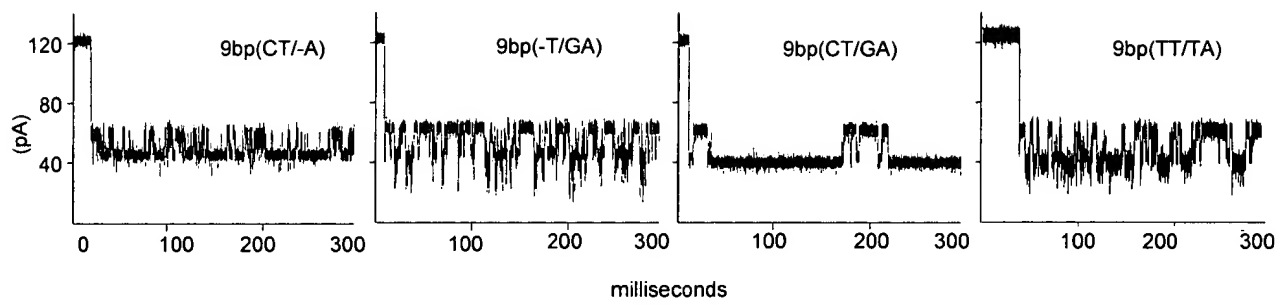


Figure 11

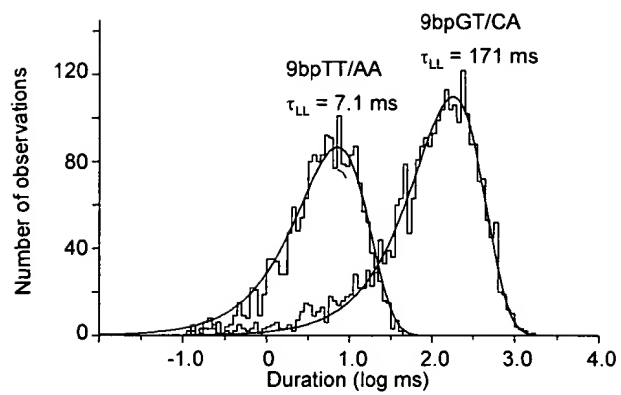


Figure 12

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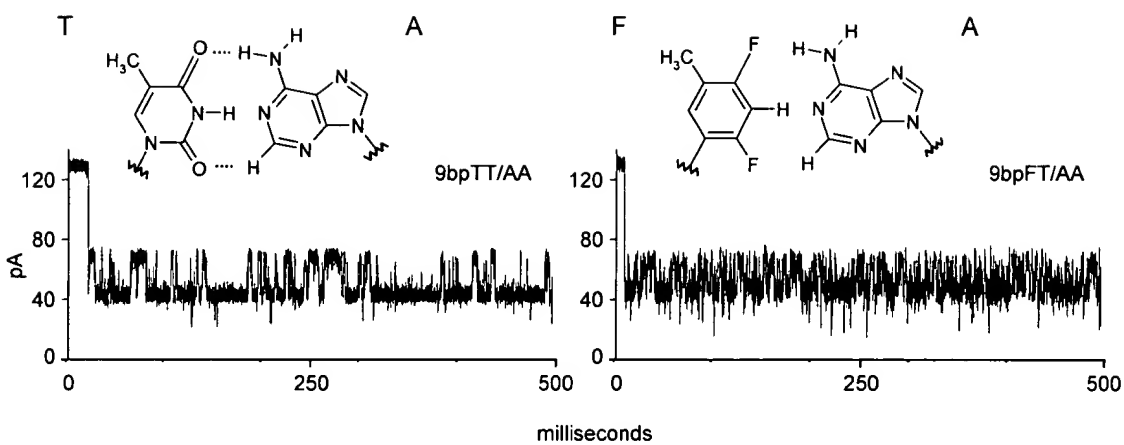


Figure 13

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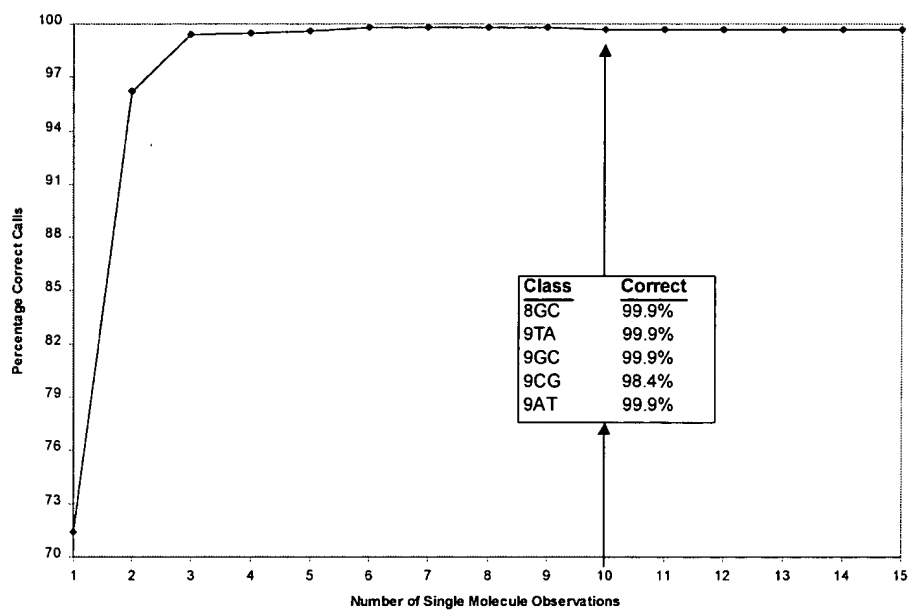


Figure 14

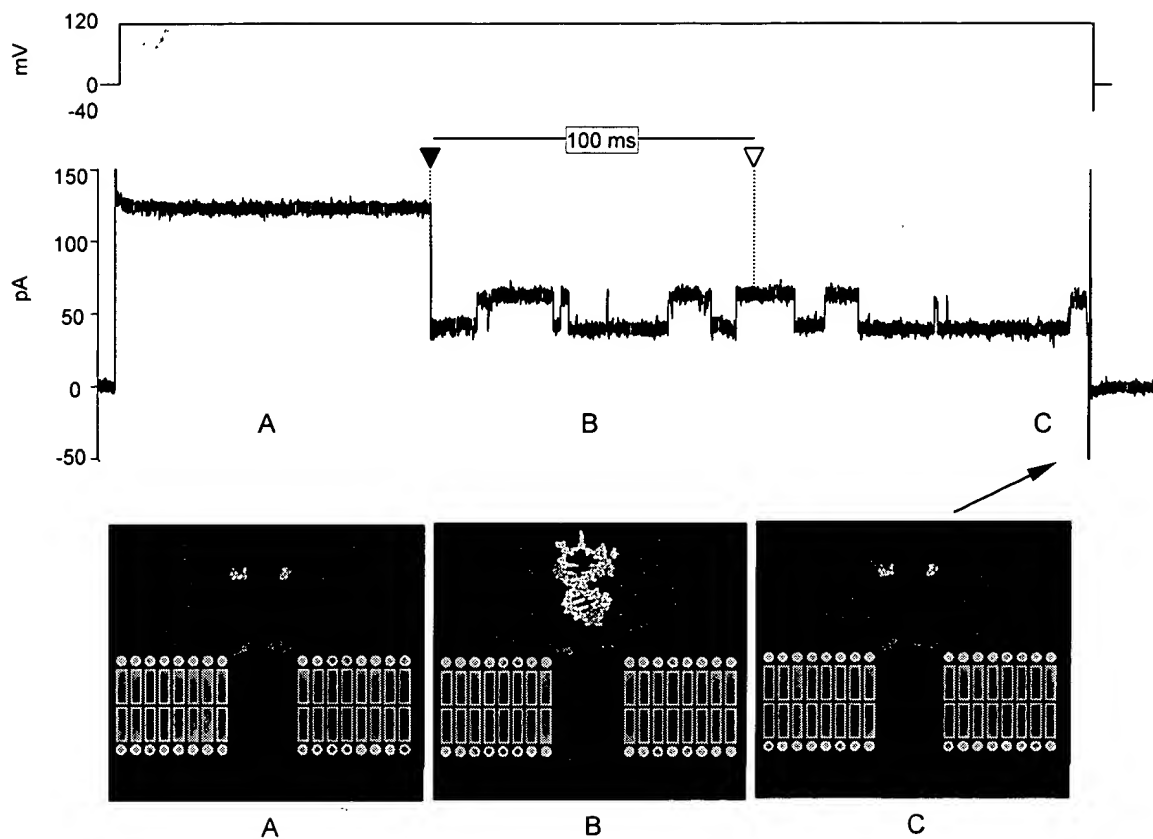


Figure 15.

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